



SEQUENCE LISTING

<110> NAKAJIMA, Hiro
NAGASAWA, Akitsu

<120> Method for giving resistance to weed control compounds to plants

<130> 0020-4764P

<140> 09/697,719

<141> 2000-10-27

<150> JP 10/120553

<151> 1998-04-30

<150> JP 10/281127

<151> 1998-10-02

<150> JP 10/330981

<151> 1998-11-20

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<151> 1999-03-02

<160> 78

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<212> DNA

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<223> Designed oligonucleotide primer to amplify bchH gene

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<223> Designed oligonucleotide primer to amplify bchH gene

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<400> 3

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<210> 4

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<400> 4

ttgtcgacaa ctgctactat ttgtacactc tatttg 36

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1 5 10 15	
ctt cgc ccc tcc ctc cat tcc cca acc tct ttc ttc acc tct ccc act	96
Leu Arg Pro Ser Leu His Ser Pro Thr Ser Phe Phe Thr Ser Pro Thr	
20 25 30	
cga aaa ttc cct cgc tct cgc cct aac cct att cta cgc tgc tcc att	144
Arg Lys Phe Pro Arg Ser Arg Pro Asn Pro Ile Leu Arg Cys Ser Ile	
35 40 45	
gcg gag gaa tcc acc gcg tct ccg ccc aaa acc aga gac tcc gcc ccc	192
Ala Glu Glu Ser Thr Ala Ser Pro Pro Lys Thr Arg Asp Ser Ala Pro	
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gtg gac tgc gtc gtc gtc ggc gga ggc gtc agc ggc ctc tgc atc gcc	240
Val Asp Cys Val Val Val Gly Gly Gly Val Ser Gly Leu Cys Ile Ala	
65 70 75 80	
cag gcc ctc gcc acc aaa cac gcc aat gcc aac gtc gtc gtc acg gag	288
Gln Ala Leu Ala Thr Lys His Ala Asn Ala Asn Val Val Val Thr Glu	
85 90 95	
gcc cga gac cgc gtc ggc ggc aac atc acc acg atg gag agg gac gga	336
Ala Arg Asp Arg Val Gly Gly Asn Ile Thr Thr Met Glu Arg Asp Gly	
100 105 110	
tac ctc tgg gaa gaa ggc ccc aac agc ttc cag cct tct gat cca atg	384
Tyr Leu Trp Glu Glu Gly Pro Asn Ser Phe Gln Pro Ser Asp Pro Met	
115 120 125	
ctc acc atg gtg gtg gac agt ggt tta aag gat gag ctt gtt ttg ggg	432
Leu Thr Met Val Val Asp Ser Gly Leu Lys Asp Glu Leu Val Leu Gly	
130 135 140	
gat cct gat gca cct cgg ttt gtg ttg tgg aac agg aag ttg agg ccg	480
Asp Pro Asp Ala Pro Arg Phe Val Leu Trp Asn Arg Lys Leu Arg Pro	
145 150 155 160	
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Val Pro Gly Lys Leu Thr Asp Leu Pro Phe Phe Asp Leu Met Ser Ile	
165 170 175	
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Pro	Pro	Gly	His	Glu	Glu	Ser	Val	Glu	Glu	Phe	Val	Arg	Arg	Asn	Leu	
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Tyr	Ala	Gly	Asp	Pro	Ser	Lys	Leu	Ser	Met	Lys	Ala	Ala	Phe	Gly	Lys	
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Val	Trp	Lys	Leu	Glu	Lys	Asn	Gly	Gly	Ser	Ile	Ile	Gly	Gly	Thr	Phe	
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Lys	Ala	Ile	Gln	Glu	Arg	Asn	Gly	Ala	Ser	Lys	Pro	Pro	Arg	Asp	Pro	
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Tyr	Ser	Leu	Thr	Tyr	Glu	Thr	Pro	Glu	Gly	Val	Val	Ser	Leu	Gln	Cys	
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Lys	Thr	Val	Val	Leu	Thr	Ile	Pro	Ser	Tyr	Val	Ala	Ser	Thr	Leu	Leu	
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cgt	cct	ctg	tct	gct	gct	gct	gca	gat	gca	ctt	tca	aag	ttt	tat	tac	1104
Arg	Pro	Leu	Ser	Ala	Ala	Ala	Ala	Asp	Ala	Leu	Ser	Lys	Phe	Tyr	Tyr	
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Pro	Pro	Val	Ala	Ala	Val	Ser	Ile	Ser	Tyr	Pro	Lys	Glu	Ala	Ile	Arg	
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tca	gaa	tcg	ttg	ata	gat	ggt	gag	ttg	aag	ggg	ttt	ggt	caa	ttg	cat	1200
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Pro	Arg	Ser	Gln	Gly	Val	Glu	Thr	Leu	Gly	Thr	Ile	Tyr	Ser	Ser	Ser	
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Asn	Ala	Gln	Asp	Pro	Phe	Val	Val	Gly	Val	Arg	Leu	Trp	Pro	Gln	Ala	
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Tyr	Val	Ser	Gly	Val	Ala	Leu	Gly	Arg	Cys	Val	Glu	Gly	Ala	Tyr	Glu	
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Arg Pro Leu Ser Ala Ala Ala Ala Asp Ala Leu Ser Lys Phe Tyr Tyr
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Pro Pro Val Ala Ala Val Ser Ile Ser Tyr Pro Lys Glu Ala Ile Arg
          370          375          380
Ser Glu Cys Leu Ile Asp Gly Glu Leu Lys Gly Phe Gly Gln Leu His
385          390          395          400
Pro Arg Ser Gln Gly Val Glu Thr Leu Gly Thr Ile Tyr Ser Ser Ser
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Leu Phe Pro Asn Arg Ala Pro Pro Gly Arg Val Leu Leu Leu Asn Tyr
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465          470          475          480
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<210> 11
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<210> 12
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<210> 13
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<213> Artificial Sequence

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<212> DNA
<213> Artificial Sequence

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<400> 14
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<210> 15
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<212> DNA
<213> Artificial Sequence

<220>
<223> Designed oligonucleotide primer to amplify Chlamydomonas PPO gene

<400> 15
aatgatgttg acccagactc ctgggacc 28

<210> 16
<211> 27
<212> DNA
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<400> 16
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  Arg Pro Thr Pro Phe Ser Val Ala Ser Pro Ala Thr Ala Ala Ser Pro
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gcg acc gcg gcg gcc cgc cgc aca ctc cac cgc act gct gcg gcg gcc 190
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Tyr Ser Ser Ser Leu Phe Pro Gly Arg Ala Pro Glu Gly His Met Leu
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Leu Leu Asn Tyr Ile Gly Gly Thr Thr Asn Arg Gly Ile Val Asn Gln
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Val Ile Lys Pro Asp Ala Pro Lys Pro Arg Val Val Gly Val Arg Val
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Trp Pro Arg Ala Ile Pro Gln Phe Asn Leu Gly His Leu Glu Gln Leu
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Asp Lys Ala Arg Lys Ala Leu Asp Ala Ala Gly Leu Gln Gly Val His
515 520 525
ctg ggg ggc aac tac gtc agc ggt gtg gcc ctg ggc aag gtg gtg gag 1630
Leu Gly Gly Asn Tyr Val Ser Gly Val Ala Leu Gly Lys Val Val Glu
530 535 540
cac ggc tac gag tcc gca gcc aac ctg gcc aag agc gtg tcc aag gcc 1678
His Gly Tyr Glu Ser Ala Ala Asn Leu Ala Lys Ser Val Ser Lys Ala
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1 5 10 15
Arg Ser Gln Ile Arg Ser Ala Ala His Val Ser Ala Lys Val Ala Pro
20 25 30
Arg Pro Thr Pro Phe Ser Val Ala Ser Pro Ala Thr Ala Ala Ser Pro
35 40 45
Ala Thr Ala Ala Ala Arg Arg Thr Leu His Arg Thr Ala Ala Ala Ala
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Thr Gly Ala Pro Thr Ala Ser Gly Ala Gly Val Ala Lys Thr Leu Asp
65 70 75
Asn Val Tyr Asp Val Ile Val Val Gly Gly Gly Leu Ser Gly Leu Val

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80		85		90		95
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Thr Glu Ala Arg	Glu Arg Val Gly Gly Asn Ile Thr Ser Met Ser Gly					
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Asp Gly Tyr Val	Trp Glu Glu Gly Pro Asn Ser Phe Gln Pro Asn Asp					
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Ser Met Leu Gln	Ile Ala Val Asp Ser Gly Cys Glu Lys Asp Leu Val					
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Phe Gly Asp Pro	Thr Ala Pro Arg Phe Val Trp Trp Glu Gly Lys Leu					
	160		165			170
Arg Pro Val Pro	Ser Gly Leu Asp Ala Phe Thr Phe Asp Leu Met Ser					
	180		185			190
Ile Pro Gly Lys	Ile Arg Ala Gly Leu Gly Ala Ile Gly Leu Ile Asn					
	195		200			205
Gly Ala Met Pro	Ser Phe Glu Glu Ser Val Glu Gln Phe Ile Arg Arg					
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Asn Leu Gly Asp	Glu Val Phe Phe Arg Leu Ile Glu Pro Phe Cys Ser					
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Gly Val Tyr Ala	Gly Asp Pro Ser Lys Leu Ser Met Lys Ala Ala Phe					
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Asn Arg Ile Trp	Ile Leu Glu Lys Asn Gly Gly Ser Leu Val Gly Gly					
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	275		280			285
Asp Pro Arg Leu	Pro Pro Lys Pro Lys Gly Gln Thr Val Gly Ser Phe					
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Arg Lys Gly Leu	Lys Met Leu Pro Asp Ala Ile Glu Arg Asn Ile Pro					
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Asp Lys Ile Arg	Val Asn Trp Lys Leu Val Ser Leu Gly Arg Glu Ala					
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Asp Gly Arg Tyr	Gly Leu Val Tyr Asp Thr Pro Glu Gly Arg Val Lys					
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Asp Leu Val Lys	Glu Gln Ala Pro Ala Ala Ala Glu Ala Leu Gly Ser					
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Ala Val Arg Glu	Glu Arg Lys Ala Ser Asp Gly Ser Val Pro Gly Phe					
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Gly Gln Leu His	Pro Arg Thr Gln Gly Ile Thr Thr Leu Gly Thr Ile					
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Tyr Ser Ser Ser	Leu Phe Pro Gly Arg Ala Pro Glu Gly His Met Leu					
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Leu Leu Asn Tyr	Ile Gly Gly Thr Thr Asn Arg Gly Ile Val Asn Gln					
	450		455			460
Thr Thr Glu Gln	Leu Val Glu Gln Val Asp Lys Asp Leu Arg Asn Met					
	465		470			475
Val Ile Lys Pro	Asp Ala Pro Lys Pro Arg Val Val Gly Val Arg Val					
	480		485			490
Trp Pro Arg Ala	Ile Pro Gln Phe Asn Leu Gly His Leu Glu Gln Leu					
	500		505			510
Asp Lys Ala Arg	Lys Ala Leu Asp Ala Ala Gly Leu Gln Gly Val His					
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Leu Gly Gly Asn	Tyr Val Ser Gly Val Ala Leu Gly Lys Val Val Glu					
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Ala Val Lys Ala
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<210> 19
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Designed oligonucleotide primer to amplify DNA fragment having partial sequence of Chlamydomonas PPO gene

<400> 19
ggtcggtgga ggggatccga tgctggtgac cg 32

<210> 20
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Designed oligonucleotide primer to amplify DNA fragment having partial sequence of Chlamydomonas PPO gene

<400> 20
gctactgctg cgagctctta ggccttgact gc 32

<210> 21
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Designed oligonucleotide primer to amplify DNA fragment having partial sequence of cucumber ferrochelatase gene

<400> 21
gctttagaat cggatcctat ggcagtggat gac 33

<210> 22
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Designed oligonucleotide primer to amplify DNA fragment having partial sequence of cucumber ferrochelatase gene

<400> 22
ggtgaacttc tatttgagct ctcaggtaaa tataag 36

<210> 23
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
 <223> Designed oligonucleotide primer to amplify Esherichia coli hemF gene

 <400> 23
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 <210> 24
 <211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Designed oligonucleotide primer to amplify Esherichia coli hemF gene

 <400> 24
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 <210> 25
 <211> 26
 <212> DNA
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 <220>
 <223> Designed oligonucleotide primer to amplify Esherichia coli hemF gene

 <400> 25
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 <210> 26
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 <212> DNA
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 <220>
 <223> Designed oligonucleotide primer to amplify Esherichia coli hemF gene

 <400> 26
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 <210> 27
 <211> 22
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Designed oligonucleotides to synthesize genes encoding random peptides
 comprising 5 amino acids

 <220>
 <221> unsure
 <222> (1)...(22)
 <223> any n = a, g, c, t, any, unknown, or other

 <400> 27
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<210> 28
 <211> 29
 <212> DNA
 <213> Artificial Sequence

 <220>
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 comprising 5 amino acids

 <220>
 <221> unknown
 <222> (1)...(29)
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 <400> 28
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 <210> 29
 <211> 22
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Designed oligonucleotide to synthesize the gene encoding the peptide HASYS

 <400> 29
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 <210> 30
 <211> 29
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Designed oligonucleotide to synthesize the gene encoding the peptide HASYS

 <400> 30
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 <210> 31
 <211> 22
 <212> DNA
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 <220>
 <223> Designed oligonucleotide to synthesize the gene encoding the peptide RASSL

 <400> 31
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 <210> 32
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 <212> DNA
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 <220>
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<400> 32
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<210> 33
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 <212> DNA
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<220>
 <223> Designed oligonucleotide to synthesize the gene encoding the peptide
 MGHASYS

<400> 33
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<210> 34
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<220>
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 MGHASYS

<400> 34
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<210> 35
 <211> 26
 <212> DNA
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<220>
 <223> Designed oligonucleotide to synthesize the gene encoding the peptide
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<400> 35
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<210> 36
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 MGRASSL

<400> 36
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<210> 37
 <211> 23
 <212> DNA
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<220>
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 MGYAGY

<400> 37
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<210> 38
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 <212> DNA
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<220>
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<400> 38
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<210> 39
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 <212> DNA
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<220>
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<400> 39
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<210> 40
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
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<400> 40
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<210> 41
 <211> 34
 <212> DNA
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<220>
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 MG(HASYS)4

<400> 41
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<210> 42
 <211> 36

<212> DNA
 <213> Artificial Sequence

 <220>
 <223> Designed oligonucleotide to synthesize the gene encoding the peptide
 MG(HASYS) 4

 <400> 42
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 <210> 43
 <211> 37
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 <220>
 <223> Designed oligonucleotide to synthesize the gene encoding the peptide
 MG(HASYS) 4

 <400> 43
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 <210> 44
 <211> 35
 <212> DNA
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 <220>
 <223> Designed oligonucleotide to synthesize the gene encoding the peptide
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 <210> 45
 <211> 30
 <212> DNA
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 <220>
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 MG(HASYS) 8

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 <210> 46
 <211> 30
 <212> DNA
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 <220>
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 MG(HASYS) 8

 <400> 46
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<210> 47
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 <212> DNA
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 <220>
 <223> Designed oligonucleotide to synthesize the gene encoding the peptide
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 <400> 47
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 <210> 48
 <211> 36
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 <220>
 <223> Designed oligonucleotide to synthesize the gene encoding the peptide
 MG(RASSL) 4

 <400> 48
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 <210> 49
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 <212> DNA
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 <220>
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 MG(RASSL) 4

 <400> 49
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 <210> 50
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 <213> Artificial Sequence

 <220>
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 <210> 51
 <211> 30
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Designed oligonucleotide to synthesize the gene encoding the peptide
 MG(RASSL) 8

<400> 51
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<210> 52
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Designed oligonucleotide to synthesize the gene encoding the peptide
 MG(RASSL)8

<400> 52
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<210> 53
 <211> 5
 <212> PRT
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<220>
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<400> 53
 His Ala Ser Tyr Ser
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<210> 54
 <211> 7
 <212> PRT
 <213> Artificial Sequence

<220>
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<400> 54
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<210> 55
 <211> 5
 <212> PRT
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<220>
 <223> Protoporphyrin IX binding protein RASSL

<400> 55
 Arg Ala Ser Ser Leu
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<210> 56
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 <212> PRT
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<220>
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<400> 56
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<220>
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<400> 57
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<210> 58
<211> 6
<212> PRT
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<220>
<223> H2TMpyP binding protein MGYAGY

<400> 58
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<210> 59
<211> 4
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<220>
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<400> 59
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<210> 60
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<220>
<223> H2TMpyP binding protein MGYAGF

<400> 60
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<210> 61
<211> 22
<212> PRT

<213> Artificial Sequence

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<223> Protoporphyrin IX binding protein MG(HASYS)4

<400> 61

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Ser His Ala Ser Tyr Ser
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<210> 62

<211> 42

<212> PRT

<213> Artificial Sequence

<220>

<223> Protoporphyrin IX binding protein MG(HASYS)8

<400> 62

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Ser His Ala Ser Tyr Ser His Ala Ser Tyr Ser His Ala Ser Tyr Ser
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His Ala Ser Tyr Ser His Ala Ser Tyr Ser
35 40

<210> 63

<211> 22

<212> PRT

<213> Artificial Sequence

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<223> Protoporphyrin IX binding protein MG(RASSL)4

<400> 63

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Leu Arg Ala Ser Ser Leu
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<213> Artificial Sequence

<220>

<223> Protoporphyrin IX binding protein MG(RASSL)8.

<400> 64

Met Gly Arg Ala Ser Ser Leu Arg Ala Ser Ser Leu Arg Ala Ser Ser
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20 25 30
Arg Ala Ser Ser Leu Arg Ala Ser Ser Leu
35 40

<210> 65
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Designed oligonucleotide primer to introduce mutation into arabidopsis PPO gene

<400> 65
gtttcagggtg tttatgttgg tgatccttca aaactg 36

<210> 66
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Designed oligonucleotide primer to amplify herbicide resistant arabidopsis PPO(A220V) gene

<400> 66
ccatgcggaa gcttatggag ttatctcttc tc 32

<210> 67
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> Designed oligonucleotide primer to amplify herbicide resistant arabidopsis PPO(A220V) gene

<400> 67
gggagattta atgtcgacca tttacttgta agcg 34

<210> 68
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Designed oligonucleotide primer to amplify Arabidopsis chloroplast ferrochelatase gene

<400> 68
gatcggttct gaaatttgga tccatgcagg c 31

<210> 69
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Designed oligonucleotide primer to amplify Arabidopsis chloroplast ferrochelatase gene

<400> 69
 cacaaaaacca acgagctcct ataggttccg g 31

<210> 70
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Designed oligonucleotide primer to amplify soybean coproporphyrinogen III oxidase gene

<400> 70
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<210> 71
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Designed oligonucleotide primer to amplify soybean coproporphyrinogen III oxidase gene

<400> 71
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<210> 72
 <211> 36
 <212> DNA
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<220>
 <223> Designed oligonucleotide primer to amplify DNA fragment having nucleotide sequence encoding the Petunia hybrida EPSPS chloroplast transit peptide and the Agrobacterium sp. strain CP4 EPSPS gene

<400> 72
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<210> 73
 <211> 32
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Designed oligonucleotide primer to amplify DNA fragment having nucleotide sequence encoding the Petunia hybrida EPSPS chloroplast transit peptide and the Agrobacterium sp. strain CP4 EPSPS gene

<400> 73
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<210> 74
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 <212> DNA

<213> Petunia hybrida EPSPS chloroplast transit peptide and Agrobacterium sp.
strain CP4 EPSPS

<220>

<221> CDS

<222> (1)...(1581)

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Leu Lys Lys Asp Ser Ile Phe Met Gln Lys Phe Cys Ser Phe Arg Ile	
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Ser Ala Ser Val Ala Thr Ala Cys Met Leu His Gly Ala Ser Ser Arg	
65 70 75 80	
ccc gca acc gcc cgc aaa tcc tct ggc ctt tcc gga acc gtc cgc att	288
Pro Ala Thr Ala Arg Lys Ser Ser Gly Leu Ser Gly Thr Val Arg Ile	
85 90 95	
ccc ggc gac aag tcg atc tcc cac cgg tcc ttc atg ttc ggc ggt ctc	336
Pro Gly Asp Lys Ser Ile Ser His Arg Ser Phe Met Phe Gly Gly Leu	
100 105 110	
gcg agc ggt gaa acg cgc atc acc ggc ctt ctg gaa ggc gag gac gtc	384
Ala Ser Gly Glu Thr Arg Ile Thr Gly Leu Leu Glu Gly Glu Asp Val	
115 120 125	
atc aat acg ggc aag gcc atg cag gcc atg ggc gcc agg atc cgt aag	432
Ile Asn Thr Gly Lys Ala Met Gln Ala Met Gly Ala Arg Ile Arg Lys	
130 135 140	
gaa ggc gac acc tgg atc atc gat ggc gtc ggc aat ggc ggc ctc ctg	480
Glu Gly Asp Thr Trp Ile Ile Asp Gly Val Gly Asn Gly Gly Leu Leu	
145 150 155 160	
gcg cct gag gcg ccg ctc gat ttc ggc aat gcc gcc acg ggc tgc cgc	528
Ala Pro Glu Ala Pro Leu Asp Phe Gly Asn Ala Ala Thr Gly Cys Arg	
165 170 175	
ctg acc atg ggc ctc gtc ggg gtc tac gat ttc gac agc acc ttc atc	576
Leu Thr Met Gly Leu Val Gly Val Tyr Asp Phe Asp Ser Thr Phe Ile	
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ggc gac gcc tcg ctc aca aag cgc ccg atg ggc cgc gtg ttg aac ccg	624
Gly Asp Ala Ser Leu Thr Lys Arg Pro Met Gly Arg Val Leu Asn Pro	
195 200 205	
ctg cgc gaa atg ggc gtg cag gtg aaa tcg gaa gac ggt gac cgt ctt	672
Leu Arg Glu Met Gly Val Gln Val Lys Ser Glu Asp Gly Asp Arg Leu	
210 215 220	
ccc gtt acc ttg cgc ggg ccg aag acg ccg acg ccg atc acc tac cgc	720
Pro Val Thr Leu Arg Gly Pro Lys Thr Pro Thr Pro Ile Thr Tyr Arg	
225 230 235 240	
gtg ccg atg gcc tcc gca cag gtg aag tcc gcc gtg ctg ctc gcc ggc	768
Val Pro Met Ala Ser Ala Gln Val Lys Ser Ala Val Leu Leu Ala Gly	
245 250 255	
ctc aac acg ccc gcc atc acg acg gtc atc gag ccg atc atg acg cgc	816

Leu	Asn	Thr	Pro	Gly	Ile	Thr	Thr	Val	Ile	Glu	Pro	Ile	Met	Thr	Arg	
			260					265					270			
gat	cat	acg	gaa	aag	atg	ctg	cag	ggc	ttt	ggc	gcc	aac	ctt	acc	gtc	864
Asp	His	Thr	Glu	Lys	Met	Leu	Gln	Gly	Phe	Gly	Ala	Asn	Leu	Thr	Val	
		275					280					285				
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Glu	Thr	Asp	Ala	Asp	Gly	Val	Arg	Thr	Ile	Arg	Leu	Glu	Gly	Arg	Gly	
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Lys	Leu	Thr	Gly	Gln	Val	Ile	Asp	Val	Pro	Gly	Asp	Pro	Ser	Ser	Thr	
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gcc	ttc	ccg	ctg	gtt	gcg	gcc	ctg	ctt	gtt	ccg	ggc	tcc	gac	gtc	acc	1008
Ala	Phe	Pro	Leu	Val	Ala	Ala	Leu	Leu	Val	Pro	Gly	Ser	Asp	Val	Thr	
			325					330						335		
atc	ctc	aac	gtg	ctg	atg	aac	ccc	acc	cgc	acc	ggc	ctc	atc	ctg	acg	1056
Ile	Leu	Asn	Val	Leu	Met	Asn	Pro	Thr	Arg	Thr	Gly	Leu	Ile	Leu	Thr	
			340					345					350			
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Leu	Gln	Glu	Met	Gly	Ala	Asp	Ile	Glu	Val	Ile	Asn	Pro	Arg	Leu	Ala	
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Gly	Gly	Glu	Asp	Val	Ala	Asp	Leu	Arg	Val	Arg	Ser	Ser	Thr	Leu	Lys	
		370				375					380					
ggc	gtc	acg	gtg	ccg	gaa	gac	cgc	gcg	cct	tcg	atg	atc	gac	gaa	tat	1200
Gly	Val	Thr	Val	Pro	Glu	Asp	Arg	Ala	Pro	Ser	Met	Ile	Asp	Glu	Tyr	
385				390					395					400		
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Pro	Ile	Leu	Ala	Val	Ala	Ala	Ala	Phe	Ala	Glu	Gly	Ala	Thr	Val	Met	
			405					410					415			
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Asn	Gly	Leu	Glu	Glu	Leu	Arg	Val	Lys	Glu	Ser	Asp	Arg	Leu	Ser	Ala	
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Val	Ala	Asn	Gly	Leu	Lys	Leu	Asn	Gly	Val	Asp	Cys	Asp	Glu	Gly	Glu	
		435				440						445				
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Thr	Ser	Leu	Val	Val	Arg	Gly	Arg	Pro	Asp	Gly	Lys	Gly	Leu	Gly	Asn	
		450				455					460					
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Ala	Ser	Gly	Ala	Ala	Val	Ala	Thr	His	Leu	Asp	His	Arg	Ile	Ala	Met	
465				470					475					480		
agc	ttc	ctc	gtc	atg	ggc	ctc	gtg	tcg	gaa	aac	cct	gtc	acg	gtg	gac	1488
Ser	Phe	Leu	Val	Met	Gly	Leu	Val	Ser	Glu	Asn	Pro	Val	Thr	Val	Asp	
			485					490					495			
gat	gcc	acg	atg	atc	gcc	acg	agc	ttc	ccg	gag	ttc	atg	gac	ctg	atg	1536
Asp	Ala	Thr	Met	Ile	Ala	Thr	Ser	Phe	Pro	Glu	Phe	Met	Asp	Leu	Met	
		500					505					510				
gcc	ggg	ctg	ggc	gcg	aag	atc	gaa	ctc	tcc	gat	acg	aag	gct	gcc	tga	1584
Ala	Gly	Leu	Gly	Ala	Lys	Ile	Glu	Leu	Ser	Asp	Thr	Lys	Ala	Ala		
		515				520						525				
tga																1587

<210> 75

<211> 33

<212> DNA

<213> Artificial Sequence

<220>
<223> Designed oligonucleotide primer to amplify DNA fragment having partial sequence of soybean PPO gene

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<210> 76
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<212> DNA
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<400> 76
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<220>
<223> PPO variant in which a region presumed to be FAD binding site of PPO

<220>
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<222> (1)...(6)
<223> any Xaa = any amino acid, unknown, or other

<400> 77
Gly Xaa Gly Xaa Xaa Gly
1 5

<210> 78
<211> 6
<212> PRT
<213> Artificial Sequence

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<223> PPO variant in which a region presumed to be FAD binding site of PPO

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Gly Gly Gly Ile Ser Gly
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